

## FIGURE 1

CGGACGCGTG GGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC  
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT  
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCCGGC  
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG  
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA  
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC  
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG  
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC  
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC  
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAACAGCCTTGCTGGGCCTGACCAAGACC  
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAACTGCCTAGCACCTGGACTTATCAA  
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC  
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT  
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT  
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTCTGC  
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT  
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTGTCT  
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT  
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA  
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG  
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

## FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS  
SRKQQNVDDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG  
SIMDVTEEVWDKTLDIRVKNAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK  
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC  
AGIVSFLCEDASYITGETVVVGGGTPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation site.**

amino acids 183-186

**N-myristoylation sites.**

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 276-278

10046-1970

# FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCGGCG  
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC  
GCGGCTGGAGGAGGAGAACCAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC  
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGC GG  
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCTCCCGGGTCTTTGTGCCTCGACCTCATAC  
AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGGCGCCTGCCTGCCTCCCTGGAGATG  
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT  
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGCCGCC  
CAGGCGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCAG  
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC  
AGAGCAGTTGGTGGGAGCAAGGCCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG  
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CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTCTG  
GCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA  
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC  
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA  
GAGATCGCGGCCCTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTACAGCCTGGAACAGCA  
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGCAGCGGCGGG  
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG  
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG  
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA  
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC  
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC  
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA  
CATGCCGCCAGCGGTGCTTCGGGCCCTCAGCCTCGTTGCTGTCCAGTGCAGATGAACCTCATGGCC  
AAGCTCAGCTACCTCTCATCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC  
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACCTGGAGATGCAGCTGGAGGAGCAGC  
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC  
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA  
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACCTGGGCCGTT  
ACATGTGGATAAACCAGGAACCTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT  
GGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC  
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGGACT  
TGGTCCACGCTCCGTTACCCCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCCC  
GAGGAACCTGAGGCAGCGGGAGGCGGCTGAGCCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG  
CCTGCCCTGGAACCTTTGGGCCTTTGTCCAAGCCCCGGCGGGAACCTGCGACGAGCCAGCCCGGGGATGA  
TTGATGTCCGGAAAAACCCCTGTAAAGCCCTCGGGGCAGACCCCTGCCTTGAGGGGAGACTCCGAGCCT  
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG  
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCAAAAGAACTGGACCCTCATTT  
AACAAAATAATATGCAAATCCCACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCTTGTG  
TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTTCAGGGGTTTG  
GCCAAGAATCATCACGAAAGGTGCGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG  
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

1003467-12704

## FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV  
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAEELLTEVNRLGSGSSAASEEEEEEEEEPPRRTL  
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAAIPGSRAVGGSKARVQARQVPPATAS  
EWRLAQAAQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE  
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE  
LERNVQLMRQQQGQLQRRLREETEQRRLAEMSKRQHRVKELELKHEQQQKILKIKTEEIA  
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE  
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS  
LRQEKDSSLKQRLEIDGKLQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR  
ASASLLSQCEMNLMAKLSYLSSETRALLCYFDKVVTLREEQHQQQIAFSELEMQLLEEQQR  
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEAIRIQALEK  
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLSPLTEG  
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG  
PLSKPRRELRRASPGMIDVRKNPL

### **Important features:**

#### **Leucine zipper pattern.**

amino acids 557-579, 794-815

#### **N-glycosylation sites.**

amino acids 133-136, 383-386

#### **Kinesin related protein Kif-4 Coiled-coil domain:**

amino acids 231-672

## FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT  
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA  
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG  
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT  
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG  
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC  
CAGGAACAGGAGGCACGTCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC  
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA  
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC  
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG  
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

10224300

## FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTDAFVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS  
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRSTRNRRHVLYP

### **Important features:**

#### **Signal sequence**

amino acids 1-21

#### **N-myristoylation sites.**

amino acids 33-39, 70-76

FIGURE 6

## FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT  
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG  
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG  
GAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT  
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG  
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG  
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTG  
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG  
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCGCCC  
GCCCGCCGGGACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA  
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG  
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG  
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT  
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC  
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CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG  
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCT  
GTGCACCGAGGAGGGGGCCGCTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA  
TCCACGTGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC  
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG  
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC  
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA  
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC  
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TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT  
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG  
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG  
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAA  
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## FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL  
GRPARDEGGSGRDWKSksGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTQPQAEALA  
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL  
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSFCERCRCCEANGEVL  
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR  
IERQAMCTRHECRQM

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 11-30

#### **Glycosaminoglycan attachment site.**

amino acids 80-83

#### **N-myristoylation sites.**

amino acids 10-15, 102-107, 103-108

#### **Cell attachment sequence.**

amino acids 114-117

#### **EGF-like domain cysteine pattern signature.**

amino acids 176-187

100346-199



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CCACCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGAACACCAGATTCTTTTC  
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GCTGCGATGTATCTGATAATACAGACCCTGTCCTTTCA

## FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI  
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PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGGRGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-15

#### **Transmembrane domain:**

amino acids 243-260

#### **N-glycosylation sites.**

amino acids 46-49, 189-192, 382-385

#### **Glycosaminoglycan attachment sites.**

amino acids 51-54, 359-362

#### **N-myristoylation sites.**

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,  
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,  
360-365, 361-366, 388-393, 408-413, 419-424

## FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG  
GCTGCGGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTTCTAGAGCCGAGGGACCCGGTGGC  
CTCGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT  
TGTCGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG  
CAGCTGGTCGCCCTCATTGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT  
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG  
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC  
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT  
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC  
ACCGCTGCATGGATAGCAGCGCCGCCCTTCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC  
TTGCCGCCCGCCGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT  
GAGATTTTTTGATCACTGTGAGAAGTTTTTAAGTGAAGTAGAAAAAATGCTACAGCTCTTT  
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT  
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTCACCTG  
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG  
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT  
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC  
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG  
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA  
GCGTACAATTACAAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTTGTACCTTATGC  
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAATTCC  
GAGTGCAGATGTTATTAAATGAAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCA  
TTTTATGAAGATCTGAAGAACCACTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA  
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTATGAGTAACTGAAGAACATTTTT  
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATT  
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC  
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTTCACTGGAGCAGCTCTCTTAAGGAGAA  
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTAC  
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAAAGTGCT  
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACCTTTAC  
AGATTGTTCTGCAGTTCTCTCTTTCTCCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC  
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT  
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA  
TGAAAATAAATATTTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT  
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC  
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTTCATTCTGT  
CACTTGGCTTCGATTTTTATATTTTCTTATTATATGAAATGTATCTTTTGGTTGTTTGATTT  
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA  
TAAAGAAAATCTTGTGACTTTAAAAAAA

## FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS  
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS  
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR  
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH  
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA  
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE  
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV  
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

### Important features:

#### Signal sequence

amino acids 1-30

#### N-glycosylation sites.

amino acids 242-246, 481-485

#### N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

#### Endoplasmic reticulum targeting sequence.

amino acids 484-489

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# FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGATCATTACGGATTTCGC  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCAGATTTTCGCAATTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGTTGTCTTGTCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACTGCGTACTTCACTCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCCTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTACCCTGGTCTGT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTGTGAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAACAACCAAAATCAGGAAG  
GTAATTTGGTTGCTGGAAGAGGGATCTTGCCCTGAGGAACCCTGCTTGTCCAACAGGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT  
TGGAAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTTCTTTTCT  
CACACAAGTTTGTAGCCTTTTTTACAAGGGAACCTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCCTTTCCGTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACCCCTCAGATGTACATACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGTCTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTTAAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCCTGTTCTCTTTTGGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG  
TGAAACGCCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTATAGTATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAAGTAGACTGCGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACCTGCTGATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTGTGTTAAC  
CTCATTTATAAAAGCTTCAAAAAAACCCA

## FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 14

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CAGGACCAGGTCCTTCCCTACGCTGGAGCAGCGGGGAGACAGCCACC**ATG**CACATCCTCTGTTGTCATGCCATGGTG  
ATCCTGCTGACGCTGGGCCCGCCTCGAGCCGACGACAGCGAGTTCCAGGCGCTGCTGGACATCTGGTTTCCGGAG  
GAGAAGCCACTGCCACC CGCCTTCCCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCCTGACTGGCTGAAGCTG  
CGCATGATCCGTTCTGAGGTGCTCCGCCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCAGCAGCTGCTGCTG  
TTCGTGCAGTTCGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCTTGGACCAGGCAGTGGCCCCAC  
GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC  
GGCGCCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCCTGCCGCCCGCCGAGACAGCACAGAGGCCA  
CCCAAACCAAAGAGCAGCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTG  
GGCCCTGAGGACGACCTGGCTGGCATGTTCCCTCCAGATTTTCCCGCTCAGCCCCGACCCCTCGGTGGCAGAGCTCC  
AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCCGCTGCTCCAGGGCAGCCCC  
GAGGTGCCGGGCATCACGGTGCCTGTCTTCAGGCCCTCGCCACCCCTGCTCAGCTCCCCACACGGCGGTGCCCTG  
GTGATGTTCCATGCACCGTAGCCACTTCCCTGGCCCTGCCCGCTGCTGCGCCAGCTCTGCCAGTACCAGCGCTGTGTG  
CCACAGGACACCGGCTTCTCCTCGCTCTTCCCTGAAGTGTCTGCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC  
GTGGAGGGCGGGGCCCTCGCGGCACAGCTCAGGATGCTTGCCAGCCAGGCCCTCAGCGGGCGCAGGCTCAGTGAT  
GTGCGAGGGGGGCTTCTGCGCCTGGCCGAGGCCCTGGCCCTTCCGTCAGGACCTGGAGGTGGTCACTCCACCGTC  
CGTGCCGTCATCGCCACCCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTCCAG  
GGGCTGATCAGAGGTGAGGTCCCCCACCCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC  
TCCCCGTTTCCAGCCTGTAAGCCCGTTGTGGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCCCTGGCTGGG  
GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCCTCCTAGTGGACTGG  
CTGGAAATGCTGGACCCCGAGGTGGTTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG  
GGCAAAGGTCAGGCCCAGGTGCCCTCGTTCCGTCCCTACCTCCTGACCCCTCTTACGCATCAGTCCAGCTGGCCC  
ACACTGCACCAGTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTTCAGACCCCTCTGCCCTCTCTGGAC  
TTCTCTCTGGGCCCTGCATCCATGTTTCCCTCGCATCTGGCAGGGGCGGGACCAGCGCACCCCGCAGAAGCGGCGGGAG  
GAGCTGGTGCCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG  
AGCCAGGACGGGGACACAGCCCGCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG  
GACGATGAGAGTGTTCAGGAAGGTGACGGAGCACCCTGTCAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGG  
AGGCGCTGCCGAGACCTTCTCTGTCAGCTCTACCTACAGCGCCCGGAGCTGCGGGTGCCCGTGGCTGAGGTCCCTA  
CTGCACAGCGAAGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTCCTT  
CGGCACACCAAGCATCCCGGGCGTTGGAGAACCGAGGGGCGGATGCGCAGCATGCGCTGCCGGAAGCTGGCGGTG  
GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCTTGCACGGCCGCACCCACCTCAACTTC  
CAGGAGTTCCGGCAGCAGAACCACCTGAGCTGCTTCCCTGCAGTGCCTGGGCCCTGCTGGAGCTGCTGCAGCCGCAC  
GTGTTCCGCAGCGAGCACCAGGGGGCGCTGTGGGACTGCCCTTCTGTCTTTCATCCGCTGCTGCTGAATTACAGG  
AAGTCTTCCCGCCATCTGGCTGCCCTTCATCAACAAGTTTGTGCAAGTTTCATCCATAAGTACATTACCTACAATGCC  
CCAGCAGCCATCTCCTTCCCTGCAGAAGCACGCCGACCCGCTCCACGACCTGTCTTTCGACAACAGTGAACCTGGTG  
ATGCTGAAATCCCCTCCTTGCAGGGCTCAGCCTGCCCGAGCAGGACGACAGGACCGACCGAGGCCCTGGACGAAGAG  
GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTCAAGCTCTCCCTGTTTACACCCCTCTGACCGCGGCCGAG  
ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC  
GAGATGTCCCGGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG  
GAGTGTTCGCCGAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTCAGCAGCGCTTTC  
CTGCCCCAGTTTCATGTACTGCCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCCTGAG  
TACGCTCTCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG  
GACCCACAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATG**TG**AGCCTGTGGCAGCCGA  
CCCCCTCCAAGCCCCGGCCCGTCCCCGTCCCCGGGGATCTCGAGGCCAAAGCCAGGAAGCGTGGGCGTTGCTGG  
TCTGTCTCCGAGGAGGTGAGGGCGCCGAGCCCTGAGGCCAGGCAGGCCAGCAATACTCCGAGCCCTGGGGTGG  
CTCCCGGGCGGGCCGTGGCATCAGGGGGCGTCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCCGG  
AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM  
IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY  
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG  
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL  
ATLLSSPHGGALVMSMHRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVLQMLQWLDSFG  
VEGGPLRAQLRMLASQASAGRRRLSDVRGGLLRALAEALAFRQDLEVVSSTVRAVIATLRSGEQ  
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVVSSLLLQEEEP  
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR  
PYLLTLFTHQSSWPTLHQIRVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPOKR  
REELVLRVQGPELISLVELILAEETRSDGDTAACSLIQARLPLLLSCCGDDESVRKVTE  
HLSGCIQQWGDVSLGRRCRDLLLQLYLQRPVPEVLLHSEGAASSSVCKLDGLIHRFI  
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLP  
MIAALLHGRTHLNFQEFQONHL  
SCFLHVLGLLELLQPHVFRSEHQALWDCLLSFIRLLNRYKSSRHLAAFINKFVQFIHKYI  
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG  
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSIDEMSRRRPEILSFFSTNLQRL  
MSSAECCRNLAFLSLALRSMQNSPSIAAAFLPTFMVCLGSQDFEVVQTALRNLPEYALLCQE  
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

#### **N-myristoylation sites.**

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,  
665-671, 698-704

#### **Amidation sites.**

amino acids 329-333, 634-638

protein sequence



## FIGURE 17

CCGGGCCATGCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGCTCCGC  
AATGGCACCTTCCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCCTCTCGCTGTCTGGTA  
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCTGGCGC  
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG  
GTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCGCTGCGAGACGGAGACGGCAA  
TCGCACCTGGGGCCGCCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC  
ACGTGCTGCACCTGCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT  
CTGCAGCCCCGCGGTGCGCGTGGGCCAGGGCCGCACCGGAGTGTCGGTGGTGATGGGCATCCC  
GAGCGTGCGGCGGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC  
TGAGCCCGCAGGAGAAGGAGGACTCGGTTCATCGTGGTGCTGATCGCCGAGACTGACTCACAG  
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT  
CCTGGAGGTCATCTCACCTCCCCCACTTCTACCCTGACTTCTCCCGCTCCGAGAGTCCT  
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC  
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA  
GCCCAACTACCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA  
TCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG  
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT  
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA  
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT  
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT  
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATAACAGCACTTCACCTGGAGAAAG  
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC  
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGCAGTGGGAACATCGAGCACCC  
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACA  
AGGAGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC  
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC  
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCGAGA  
TCTTCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA  
GCCACATTTCTGGGGGTGTGCTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCCAA  
AGGGTTCTGCCGTGGCGTCGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCCGAGGCCCTA  
GGAGCTGGTGCTGCCCCCGCCCGCCGGGCCGCGGAGGAGGCAGGCGGCCCCACACTGTGCC  
TGAGGCCCGGAACCGTTTCGCACCCGGCCTGCCCCAGTCAGGCCGTTTTAGAAAGAGCTTTTAC  
TTGGGCGCCCGCCGTCTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT  
TTTTATTCTTGGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG  
ACTTGTAAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAA

## FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRHLHAAEQESLKRSK  
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA  
KESSLQPAVRVGQGRGTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE  
TDSQYTSAVTENIKALFPTEIHSGLLLEVISPSPHFYPDFSRRLRESFGDPKERVVRWRTKQNL  
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL  
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT  
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD  
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS  
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

### **Important features:**

#### **Signal sequence**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 5-9, 87-91, 103-107, 465-469

#### **N-myristoylation sites.**

amino acids 6-12, 136-142, 370-376, 509-515

100316-12701